

SEQUENCE LISTING

<110> Shi, Jinrui
Beach, Larry
Wang, Hongyu
Rafalski, Antoni J.
Rebecca E. Cahoon

<120> Novel Inositol Polyphosphate Kinase
Genes and Uses Thereof

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<151> 2001-01-12

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Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp
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Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu
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His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro
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Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu
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Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu
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Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys

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Lys Tyr Leu Ala Lys Asp Arg Gly Thr Thr Ser Val Leu Leu Gly Phe			
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cgc gtc ttg cgt ccg agt cgt cgg ccc cga ggg cgc cgt gtg gcg gac			545
Arg Val Leu Arg Pro Ser Arg Arg Pro Arg Gly Arg Arg Val Ala Asp			
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Gly Ala Pro Gly Gly Glu Gly Tyr Gly His Arg Arg Arg Pro Pro Arg			
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gct ccg gcg cta cgt gtc atc cgc ttg ccg acg agg gga tgg act gcg			641
Ala Pro Ala Leu Arg Val Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala			
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Arg Ser Arg Arg Arg Cys Thr Glu Glu Lys Val Glu Ser Cys His Ser			
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Cys Ala Ser Ser Arg His Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser			
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act cgg cgt cga ttc ttc tgg gct atg atg ctg ctg cag tgc cag cag			785
Thr Arg Arg Arg Phe Phe Trp Ala Met Met Leu Leu Gln Ser Gln Gln			
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Ala Glu Val Gly Val Gly *			
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35 40 45			
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr			

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Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly				
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Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp				
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Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp				
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Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser				
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Arg Arg Pro Arg Gly Arg Arg Val Ala Asp Gly Ala Pro Gly Gly Glu				
145		150		155
Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val				
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Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys				
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Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His				
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Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe				
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Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro	
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Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala	
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ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc	250
Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe	
	55 60 65
ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg	298
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly	
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Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu
85 90 95

gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg 394
Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro
100 105 110

agt tgc ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg 442
Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly
115 120 125 130

acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc 490
Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val
135 140 145

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Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala
150 155 160

atg gac acc gtc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc 586
Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser
165 170 175

gct tgc cga cga ggg gat gga ctg cgc gct cgc ggc ggc ggt gta cgg 634
Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly Val Arg
180 185 190

agg aaa agg tgg agt ctt gtc act gct gcg cga gct caa ggc gtg gtt 682
Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly Val Val
195 200 205 210

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Arg Gly Ala Ala Ser Val Pro Leu Leu Leu Gly Val Asp Ser Ser Gly
215 220 225

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Leu *

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Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
35 40 45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr

50 55 60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65 70 75 80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
85 90 95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
100 105 110
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp
115 120 125
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
130 135 140
Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
145 150 155 160
Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val
165 170 175
Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly
180 185 190
Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly
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Ser Gly Leu
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Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala
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Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro
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ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala
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Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe
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ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly
70 75 80

gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag	346
Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu	
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Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly	
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Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val	
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Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala	
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Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser	
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Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val Tyr Gly	
180 185 190	
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Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe	
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Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly	
215 220 225	
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Tyr Asp Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Gly Val Thr	
230 235 240	
gtg aag ctg gtg gac ttt gcc cat gtg gcc gag ggt gat ggg gtg att	826
Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile	
245 250 255	
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Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser	
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[illegible]

<213> Zea mays

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Ser	Lys	Leu	Gly	Pro	Leu	Ile	Asp	Gly	Ser	Gly	Leu	Phe	Tyr	Lys	Pro		
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Leu	Gln	Ala	Gly	Asp	Arg	Gly	Glu	His	Glu	Val	Ala	Phe	Tyr	Glu	Ala		
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Phe	Ser	Ala	His	Ala	Ala	Val	Pro	Ala	Arg	Ile	Arg	Asp	Thr	Phe	Phe		
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ccc	cgg	ttc	cac	ggc	acg	cga	ctc	ctc	ccc	acc	gag	gcg	cag	ccc	ggg		297
Pro	Arg	Phe	His	Gly	Thr	Arg	Leu	Leu	Pro	Thr	Glu	Ala	Gln	Pro	Gly		
			70					75					80				
gag	ccg	cat	cct	cac	ctc	gtc	ctc	gac	gac	ctc	ctc	gcg	ggg	ttt	cag		345
Glu	Pro	His	Pro	His	Leu	Val	Leu	Asp	Asp	Leu	Leu	Ala	Gly	Phe	Gln		
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gcg	ccc	tgc	gtc	gca	gac	atc	aag	atc	ggc	gcc	atc	acg	tgg	cca	ccg		393
Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr	Trp	Pro	Pro		
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Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala	Lys	Cys	Leu	Ala	Lys	Asp	Arg	Gly		
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Thr	Thr	Ser	Val	Leu	Leu	Gly	Phe	Arg	Val	Ser	Gly	Val	Arg	Val	Val		
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Gly	Pro	Glu	Gly	Ala	Val	Trp	Arg	Thr	Glu	Arg	Pro	Glu	Val	Lys	Ala		
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Tyr	Asp	Ala	Ala	Ala	Val	Ala	Ala	Gly	Gly	Asp	Gly	Gly	Gly	Val	Thr		
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Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile
245 250 255

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Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser
260 265 270

gac att gtt ccg gag act cct cat acg cag cct ttg ggt cct tct taa 921
Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro Ser *
275 280 285

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35 40 45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
50 55 60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65 70 75 80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
85 90 95
Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
100 105 110
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp
115 120 125
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
130 135 140
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
145 150 155 160
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val
165 170 175
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val
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Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala
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Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu
210 215 220
Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly
225 230 235 240

Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly
245 250 255
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Ala Lys Asp Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe
15 20 25
tac aag ccc ctc cag acc aac aaa gac gac gac acc cgc ggc tcc acc 146
Tyr Lys Pro Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr
30 35 40 45
gaa ctc tcc ttt tac acc tct ctc gcc gcc gcc gcc cac gac tac tcc 194
Glu Leu Ser Phe Tyr Thr Ser Leu Ala Ala Ala Ala His Asp Tyr Ser
50 55 60
atc cgc tcc ttc ttc ccc gcc ttt cac ggc acc cgc ctc ctg gac gcc 242
Ile Arg Ser Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala
65 70 75
tcc gac ggc tcc ggt ccc cac cct cac ctg gtc ctg gag gac ctc ctc 290
Ser Asp Gly Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu
80 85 90
tgc ggc tac tcc aaa ccc tcc gtc atg gac gta aag atc ggc tcc aga 338
Cys Gly Tyr Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg
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Thr Trp His Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys
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aag gac aga gag tcc tct agc ttg ccc ttg ggt ttc aga atc tcg gga 434
Lys Asp Arg Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly
130 135 140
gtc aag gac tct atc tcc tcc tgg gaa cct acc agg aaa tct ctc cag 482
Val Lys Asp Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln

145	150	155	
tgt cta tcc gcc cat ggt gtt gca ctt gtt ctc aac aag ttc gtt tcc			530
Cys Leu Ser Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser			
160	165	170	
tct aat aat atc aac cat gat gat cat cat ccc gat tgc gct ttc gca			578
Ser Asn Asn Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala			
175	180	185	
acg gag gtc tac ggc gcc gtt ttg gag cgc ttg cag aag ctc aag gac			626
Thr Glu Val Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp			
190	195	200	205
tgg ttc gag gtt cag acg gtg tat cac ttc tat tct tgt tct gtt ctt			674
Trp Phe Glu Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu			
210	215	220	
gtg gtg tac gag aag gat cta ggg aaa ggg aaa gct acc aac cct ctg			722
Val Val Tyr Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu			
225	230	235	
gtc aaa ctc gtt gac ttt gca cac gtg gtg gac gga aac ggt gtc att			770
Val Lys Leu Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile			
240	245	250	
gat cac aac ttc ttg ggt ggc ctt tgt tcc ttc atc aag ttc ctc aag			818
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys			
255	260	265	
gat atc cta gca gta gca tgt ctt cac aag tga ctgattttca tcgagttaat			871
Asp Ile Leu Ala Val Ala Cys Leu His Lys *			
270	275		
cttattccta tcagaaaata attatgcttg aattagtgtc gcagactaac tgtttgaagt			931
actgtcagaa acaaaataat aatatggact gagaggcaat cttgttctgc taaactccct			991
ttcaagttgc tgtcagatac tagccgtccc ttttcctttt tcatattctg tcaaagttag			1051
tcatttaata ataataacaa tgtccttcaa ctccaaaaaa aaaaaaaaaa aaaa			1105
<210> 10			
<211> 279			
<212> PRT			
<213> Glycine max			
<400> 10			
Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys Ala Lys Asp			
1	5	10	15
Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro			
20	25	30	
Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser			
35	40	45	
Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser			
50	55	60	
Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly			
65	70	75	80
Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr			
85	90	95	
Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His			

70	75	80	
cct cac ctg gtt ctg gag gat ctc gtc tcg ggt cgc acg aac cca tct			406
Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro Ser			
85	90	95	
ctc atg gac atc aag act gga tcc aga aca tgg tat ccg gag gcc tct			454
Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala Ser			
100	105	110	
gag gag tac atc caa aag tgc tta gag aaa gat cga aat agc aca agc			502
Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr Ser			
115	120	125	
gtt tca ttg ggt ttt agg att tct ggg cta agg gta tat caa aat agc			550
Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn Ser			
130	135	140	145
gaa gct gga ttt tgg caa cct gag aag aag gtt gtt tat agc ttt aat			598
Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe Asn			
150	155	160	
gcg gac ggt gtc agg tcg gct ctg agg aag ttt gtt tct tcc aac ttg			646
Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn Leu			
165	170	175	
tct ctg ggt cca aat gtg gat ccg gat tgt ttg tat gca tca aaa gtt			694
Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys Val			
180	185	190	
tac tgt cac cgg ggt gga att ttg gca caa ttg ctt cag ctg aag gaa			742
Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys Glu			
195	200	205	
tgg ttt gag gtt cag acg aat tat cac ttc tat tct tgt tca ctc att			790
Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu Ile			
210	215	220	225
atc tta tat gac agg gag tct gct ttg gac ggc tgt gca cac ccg aaa			838
Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro Lys			
230	235	240	
gtt aaa ctg gtg gac ttt gca cat gtg atg gat ggc cac ggc gtg atc			886
Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val Ile			
245	250	255	
gat cac aac ttc ttg ggt ggc ctc tgt tct gta atc aag ttt ata cgt			934
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile Arg			
260	265	270	
gac att gct gat gaa gat aac aag tgt gca aag tgc gaa gtc aat ctt			982
Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn Leu			
275	280	285	
gga ttg aaa gaa aat ggc ttc tat aag agc agc acg gaa cca gag ctt			1030
Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu Leu			
290	295	300	305

gat cac gag gcc tgc tag tggaaactgg agaataactg cattcatgca 1078
 Asp His Glu Ala Cys *
 310

ttcctgcatt cctgctctga caagtgggtc agaatgggta taataacagt ctatttttagt 1138
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<210> 12
 <211> 310
 <212> PRT
 <213> Eucalyptus grandis

<400> 12
 Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly
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 Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro
 20 25 30
 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser
 35 40 45
 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro
 50 55 60
 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro
 65 70 75 80
 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro
 85 90 95
 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala
 100 105 110
 Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr
 115 120 125
 Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn
 130 135 140
 Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe
 145 150 155 160
 Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn
 165 170 175
 Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys
 180 185 190
 Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys
 195 200 205
 Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu
 210 215 220
 Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro
 225 230 235 240
 Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val
 245 250 255
 Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile
 260 265 270
 Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn
 275 280 285
 Leu Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu
 290 295 300
 Leu Asp His Glu Ala Cys
 305 310

<210> 13
 <211> 1020
 <212> DNA

<213> Parthenium argentatum

<220>

<221> CDS

<222> (21)...(908)

<400> 13

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gcacgagaac ttcttcagac atg ctc aag gcc cca gat cat cag gtt gct gga      53
                Met Leu Lys Ala Pro Asp His Gln Val Ala Gly
                  1                5                10

cat gaa gct ggg ctc ggg aag ctt ggc cca ctc att gat gat tca ggc      101
His Glu Ala Gly Leu Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly
              15                20                25

cgg ttt tac aaa cca ctg cag ggt gat aac cgt ggg tca gaa gaa gta      149
Arg Phe Tyr Lys Pro Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val
              30                35                40

gcc ttt tat gaa tca ttt tct tct aac aat aat att cca gaa cac ata      197
Ala Phe Tyr Glu Ser Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile
              45                50                55

cgc aaa ttc ttt cct ata tat tat ggc acc aaa atc atg aag gca tcc      245
Arg Lys Phe Phe Pro Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser
              60                65                70                75

act ggc tct gac cat cct cac atg gtg ttg caa gat ctt aca tca gct      293
Thr Gly Ser Asp His Pro His Met Val Leu Gln Asp Leu Thr Ser Ala
              80                85                90

cat gtc aac cca tct gta atg gac atc aaa atc ggg tcc aga aca tgg      341
His Val Asn Pro Ser Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp
              95                100                105

gcg cca gaa gct tcc gag gcg tac att gca aaa tgc tta aaa aag gat      389
Ala Pro Glu Ala Ser Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp
              110                115                120

agg gaa agc aca agt att cca ttg gga ttc agg atc tcc ggg ctg caa      437
Arg Glu Ser Thr Ser Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln
              125                130                135

gtc tat atc gat gat ggg tca ggg ttt tat aag cct cat aga aat tac      485
Val Tyr Ile Asp Asp Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr
              140                145                150                155

atg cgt aaa acc ggc cca gct gat gtt aga cta ctt ctt agg aaa ttt      533
Met Arg Lys Thr Gly Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe
              160                165                170

gtt tct tct aac ccg tct gca gag atg gaa atg cgc aca ggc cta ggc      581
Val Ser Ser Asn Pro Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly
              175                180                185

ccg gat tgt tct tta gca tct ttt gtt tat ggt ggg cct aat ggg ata      629
Pro Asp Cys Ser Leu Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile
              190                195                200
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tta gct caa ctg atg gaa ttg aag aca tgg ttt gaa gat caa aca att	677
Leu Ala Gln Leu Met Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile	
205 210 215	
tac cac ttc tat gct tgt tct ttt ttg ttc atc ttt gaa aag agg ttg	725
Tyr His Phe Tyr Ala Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu	
220 225 230 235	
gtg tta aaa ggt gct cgg tca aac gca gaa gtc aaa ctt att gat ttt	773
Val Leu Lys Gly Ala Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe	
240 245 250	
gct cat gtt aca gat ggt aat ggt gtt att gat cac aat ttc ttg ggt	821
Ala His Val Thr Asp Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly	
255 260 265	
ggg ctc tgt tct ttg ata aag ttc att tct gac ata ctt tcg gag aca	869
Gly Leu Cys Ser Leu Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr	
270 275 280	
aaa gat tgt aat ggt aca aac ggt cag gtt gaa ctt tga aactctcttc	918
Lys Asp Cys Asn Gly Thr Asn Gly Gln Val Glu Leu *	
285 290 295	
ttgttgcttt tcttcaataa tttatcatga cagtgtttaa ttgtaaagat attcgcttac	978
cggaatatat cttgggttatg agtgaaaaaa aaaaaaaaaa aa	1020

<210> 14
 <211> 295
 <212> PRT
 <213> Parthenium argentatum

<400> 14

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Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser	
35 40 45	
Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro	
50 55 60	
Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His	
65 70 75 80	
Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser	
85 90 95	
Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser	
100 105 110	
Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser	
115 120 125	
Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp	
130 135 140	
Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly	
145 150 155 160	
Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro	
165 170 175	
Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu	
180 185 190	

Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met
 195 200 205
 Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala
 210 215 220
 Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala
 225 230 235 240
 Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp
 245 250 255
 Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu
 260 265 270
 Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr Lys Asp Cys Asn Gly
 275 280 285
 Thr Asn Gly Gln Val Glu Leu
 290 295

<210> 15
 <211> 899
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (89)...(424)

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 cacccttgc tcccatagtc cccatacc atg ccc gac ctc cac ccg ccg gag 112
 Met Pro Asp Leu His Pro Pro Glu
 1 5
 cac caa gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc cca ctc 160
 His Gln Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu
 10 15 20
 atc gac ggc tct ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt 208
 Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg
 25 30 35 40
 ggg gag cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc 256
 Gly Glu His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala
 45 50 55
 gtc ccg gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac ggc acg 304
 Val Pro Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr
 60 65 70
 cga ctc ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg tac ctc 352
 Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro Tyr Leu
 75 80 85
 gtc ctc gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac 400
 Val Leu Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp
 90 95 100
 atc aag atc ggt gcc atc acg tga ccatgagcga tctgctcgga ttccacgtct 454
 Ile Lys Ile Gly Ala Ile Thr *
 105 110

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ccggcgctccg agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc cctgaggtga 514
aggctatgga cattgtcggc gtccgccgcg tgctccggcg ctgcatgtca tccgcttgcc 574
ggcgagggga tggactgcgc gctcgcggcg gcggtgtacg gaggaaaagg tggagtcttg 634
tcacagctgc gcgagctcaa ggcgtgggtc gaggggcaga ctctgttcca cttctactcg 694
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gtaacagtga agctgggtga ccttgcccat gtggccgagg gtgatggggg gattgaccac 814
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ccttagacgc agcaaggcg aattc 899

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<210> 16
 <211> 111
 <212> PRT
 <213> Zea mays

<400> 16

Met	Pro	Asp	Leu	His	Pro	Pro	Glu	His	Gln	Val	Ala	Gly	His	Arg	Ala
1				5					10					15	
Ser	Ala	Ser	Lys	Leu	Gly	Pro	Leu	Ile	Asp	Gly	Ser	Gly	Leu	Phe	Tyr
			20					25					30		
Lys	Pro	Leu	Gln	Ala	Gly	Asp	Arg	Gly	Glu	His	Glu	Val	Ala	Phe	Tyr
			35				40					45			
Glu	Ala	Phe	Ser	Ala	His	Ala	Ala	Val	Pro	Ala	Arg	Ile	Arg	Asp	Thr
			50				55				60				
Phe	Phe	Pro	Arg	Phe	His	Gly	Thr	Arg	Leu	Leu	Pro	Thr	Glu	Ala	Gln
65					70					75				80	
Pro	Gly	Glu	Pro	His	Pro	Tyr	Leu	Val	Leu	Asp	Asp	Leu	Leu	Ala	Gly
				85					90					95	
Phe	Glu	Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr	
			100					105					110		

<210> 17
 <211> 643
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (1)...(643)
 <223> n = A,T,C or G

<400> 17

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ccgacctcca	cccgccggag	caccaagtcg	ccggtcaccc	cgccctccgc	agcaagctgg	180
gcccgtcat	cgacggctcc	ggcctcttct	acaagccgct	ccaggccggc	gaccgtgggg	240
agcacgaggt	cgcttctat	gaggcggtct	ccgcccacgc	cgncgtccc	gcccgcattc	300
gagacacctt	cttcccccg	ttccacggca	cgcgactcct	ccccaccgag	gcgcagcccg	360
gggagccgca	tccgcacctc	gtcctcgacg	acctcctcgc	ggggtttgag	gcgccttgcg	420
tcgcagacat	caagatcggc	gccatcacgt	ggccacogag	ttcgccggag	ccctacatcg	480
ncaagtacct	ngccaaggac	cgcgggacca	cgagcggtct	gctcggattc	cgcgctcttc	540
gtccgagtcg	tcggccccga	gggcgcgctg	tggcgagcgg	agcgcccccg	gggtgaangc	600
tatggacacc	cgtcggnngc	cggcgngtgc	ttcggnngct	acg		643

<210> 18
 <211> 519
 <212> DNA

206070 "462400"

<213> Zea mays

<220>

<221> misc_feature

<222> (1)...(519)

<223> n = A,T,C or G

<400> 18

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tcgcagcagg	cggangtggg	ggtggggtaa	cagtgaagct	ggtggacttt	gccccatgtg	180
ccgaggggtga	tgggggtgatt	gaccacaact	tcttgggcgg	gctctgctan	ctgatcaagt	240
ttgtttctga	cattgttcca	gagactcctc	agacgcagcc	tttgggtcct	tcttaagaaa	300
agatcctggc	atttttcgatt	tgataacaaa	ggaancactt	tcagctgcca	aaaaaaaaanc	360
accagtgaag	atgaaaataa	cattattgag	gaaagtccg	atnataaccc	accanattna	420
aaaaaaaaaag	gtcccaaatt	tccgaaaatn	tgatctttaa	gaataatctc	ctgaaaaacan	480
aattataaaa	cgtgaaaacc	ccggctncnt	catttacnc			519

<210> 19

<211> 353

<212> DNA

<213> Zea mays

<220>

<221> misc_feature

<222> (1)...(353)

<223> n = A,T,C or G

<400> 19

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gtggactttg	cccatgtggc	cgaggggtgat	gggggtgatt	tgaccacaac	ttcctgggcg	180
agctctgcta	gctgatcaag	ttccgtttct	tgacattggt	ccaganactc	cttagacgcc	240
agcctttggg	tccttcctta	aaaaaagatc	cctgacnttt	ttgatttgat	tacnaaggaa	300
acactttcca	cttgccnaaa	aaaaaagccc	ntgaggatta	aaaaattaac	ntt	353

<210> 20

<211> 3416

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (72)...(407)

<400> 20

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	Met	Pro	Asp	Leu	His	Pro	Pro	Glu	His	Gln	Val	Ala	Gly
	1				5					10			
cac cgc	gcc tcc	gcc agc	aag ctg	ggc cca	ctc atc	gac gac	tct ggc	158					
His Arg	Ala Ser	Ala Ser	Lys Leu	Gly Pro	Leu Ile	Asp Asp	Ser Gly						
	15			20			25						
ctc ttc	tac aag	ccg ctc	cag gcc	ggc gac	cgt ggg	gag cac	gag gtc	206					
Leu Phe	Tyr Lys	Pro Leu	Gln Ala	Gly Asp	Arg Gly	Glu His	Glu Val						
	30		35		40		45						

gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc 254
Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile
50 55 60

cga gac acc ttc ttc ccc cgg ttc cac ggc acg cga ctc ctc ccc acc 302
Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr
65 70 75

gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc gac gac ctc 350
Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu
80 85 90

ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag atc ggt gcc 398
Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala
95 100 105

atc acg tga ccacgagcgt tctgctcgga ttccgcgtct ccggcgctccg 447
Ile Thr *
110

agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc ccggagggtga aggctatgga 507
cattgtcggc gtccgccgcg tgcctcggcg ctacgtgtca tccgcttgcc gacgagggga 567
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gaaaacagta aaagtatgca ggcagtatga gggacacaca tagtttactg aaactccctt 1227
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tccaaacaaa cactatctgc ggcctcggta agtaacgagc ctccgctcgg ctcgctcctc 1347
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aaaatataaa ttaatcatct atttagtacc tataatatat gttaattaaa atttatataa 1587
caaaaatggt gttgtttgag ccagctcgcg agctgaactg gctcgcctctg gctcgcctctt 1647
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aatgagatgc tctacttata tacattatta ttacatccct ctgaagttgt atcttcagaa 2607
gttcacattg acagtatttg cttcctcttg ccatacttac ccatcatggc ccatgggggtg 2667

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tctatcttat catgccatct tcaaagaatg gcatcatggt aacaaaaatg aatgagaaat 2727
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gctctatagc acttcttgcg aaaagtggga atctttctct aactgaatta atgttagaat 2847
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ctgttgccgt gtactcaggc tttatttcaa caagatttaa atatgagatg tagagtgtt 3267
gatgtacatc acttcactaa tcatgaaatc tgtagaaggc gaaactacta gccatatatg 3327
atatgcataa tccgtgtggt aaacattatc aatatcacac aaattatttc taatgggttt 3387
tgaattatca aaaaaaaaaa aaaaaaaaaa 3416

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<210> 21
 <211> 111
 <212> PRT
 <213> Zea mays

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<400> 21
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
 1          5          10          15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Leu Phe Tyr
          20          25          30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
          35          40          45
Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr
          50          55          60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65          70          75          80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
          85          90          95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
          100          105          110

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<210> 22
 <211> 1448
 <212> DNA
 <213> Parthenium argentatum

<220>
 <221> CDS
 <222> (52)...(1020)

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<400> 22
gcacgaggca cactcaatgg ctccgatgct cagaggccaa cggagggtac c atg ctg 57
                                     Met Leu
                                     1

cca gct cca gct gtt cct aat ggc acg ggt gct ccg ctt aag gac gaa 105
Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys Asp Glu
 5          10          15

cct tcc aac ccc gat cag gcg cag cac cag cct gac gag cgc gtt caa 153
Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg Val Gln
20          25          30

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cac ttc atc ctt ctt gaa gac ctt act gct ggc atg aca agg cct tgt	201
His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg Pro Cys	
35 40 45 50	
gtc tta gac ttg aag atg ggt acg cgc cag tat ggt gtg gaa gcc gat	249
Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu Ala Asp	
55 60 65	
gag aag aaa cag cgg tct caa cgg cgc aag tgt cag atg acc acc agt	297
Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr Thr Ser	
70 75 80	
gct caa ctc ggc gtg cga gtc tgc ggt atg caa att tgg aac gcc aag	345
Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn Ala Lys	
85 90 95	
acc cag agc tac atc ttc gag gac aag tac ttc ggt cga gat ctg aaa	393
Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp Leu Lys	
100 105 110	
gca gga aaa gaa ttt cag gac gcg ctt aag cgc ttt ttt tgg gat ggg	441
Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp Asp Gly	
115 120 125 130	
acg agc tac aaa gca gca aac aga cac ata ccc gtc ata ttg gag aag	489
Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu Glu Lys	
135 140 145	
atc agc caa ctg gaa cgc atg ata cga aaa ctt cca gga tac aga ttc	537
Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr Arg Phe	
150 155 160	
tac gcg agt agt ttg ttg atg ctc tat gat cgt ggg gac ggt gag tcg	585
Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly Glu Ser	
165 170 175	
aag gag aaa gac gca gca ccc tct tta cct aac ggc ttg tcg aac ccg	633
Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser Asn Pro	
180 185 190	
agc aac gaa gac gtt tca aca ata cca tct gga ctt aca tca cca ggg	681
Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser Pro Gly	
195 200 205 210	
ccg aca gtc gct tct aaa ccg tca ccc aag aag cac gga gag atc aag	729
Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu Ile Lys	
215 220 225	
ctg aaa att gtc gac ttt gcc aac tgc gtg act gca gaa gac cct cta	777
Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp Pro Leu	
230 235 240	
cca gac gac tta cct tgt cca cct gaa aat ccc gac ggc atc gat aga	825
Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile Asp Arg	
245 250 255	
ggg tac ctc cgt ggc ctc cga tca cta cgc ctc tac ttc caa cgc att	873
Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln Arg Ile	

260 265 270

tgg aat gac atc aac gag gaa tgg gtc gaa cga ggc gag ggc gag ggc 921
 Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly Glu Gly
 275 280 285 290

atg gcg cga aat cat cac cat ggc cct ggt tta ggt gag gtt ggt gcg 969
 Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val Gly Ala
 295 300 305

ggc tgg atg gat gat gct ggt ggt gag gat aca ggc tac gcc agt ttc 1017
 Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala Ser Phe
 310 315 320

taa agaagaggag gaacagcaaa gctgcccacg ctcgacagaa gtcggacagt 1070
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cgatattgat acgtccatcc cttttccctt cccttcattt ccacgttcag tctatttcac 1130
 attgtgtgca ttttggttg caagcatggt gttttggtgc ataatggtaa gacaaaggt 1190
 aatgaaattg gcaactcttt tggcatgcat cggcgagca ttttatgggc ggtcagaacc 1250
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 aaaaaaaaaa aaaaaaaaaa 1448

<210> 23
 <211> 322
 <212> PRT
 <213> Parthenium argentatum

<400> 23
 Met Leu Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys
 1 5 10 15
 Asp Glu Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg
 20 25 30
 Val Gln His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg
 35 40 45
 Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu
 50 55 60
 Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr
 65 70 75 80
 Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn
 85 90 95
 Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp
 100 105 110
 Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp
 115 120 125
 Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu
 130 135 140
 Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr
 145 150 155 160
 Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly
 165 170 175
 Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser
 180 185 190
 Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser
 195 200 205

Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu
 210 215 220
 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp
 225 230 235 240
 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile
 245 250 255
 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln
 260 265 270
 Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly
 275 280 285
 Glu Gly Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val
 290 295 300
 Gly Ala Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala
 305 310 315 320
 Ser Phe

<210> 24
 <211> 2270
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (3)...(953)

<400> 24
 cc acg cgt ccg cga aaa ttg aga aac att gtt cag tgg acg ccg ttc 47
 Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe
 1 5 10 15
 ttt caa act tac aaa aaa cag agg tat cca tgg gta cag cta gcc gga 95
 Phe Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly
 20 25 30
 cac caa ggc aat ttc aaa gcc ggt ccg gaa cct ggt acg atc ctc aag 143
 His Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys
 35 40 45
 aaa ctt tgt ccc aaa gaa cag ttg tgc ttc caa gtg ctg atg aag gac 191
 Lys Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp
 50 55 60
 gtt ctg aga ccg tac gtg ccc gaa tac aag ggc cac ttg act acc gac 239
 Val Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp
 65 70 75
 gac gga gac cta tat ctt cag cta gaa gac ttg ttg ggt gac ttc act 287
 Asp Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr
 80 85 90 95
 tcg ccg tgc gtc atg gac tgc aag atc ggc gtc agg acg tat ctg gaa 335
 Ser Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu
 100 105 110
 gag gaa ctg gcg aaa gcc aaa gag aaa ccc aag ttg aga aaa gac atg 383
 Glu Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met

115	120	125	
tac gaa aaa atg att cag ata gac ccc aac gca cca tcg gag gag gaa			431
Tyr Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu			
130	135	140	
cac cga ctg aag ggt gtg aca aaa ccg agg tac atg gtt tgg agg gag			479
His Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu			
145	150	155	
acg att tcg tcc acg gcc acg ttg ggc ttc cgg atc gag ggg atc aag			527
Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys			
160	165	170	175
aaa agc gat gga aaa tcg agc aag gac ttc aag acg aca aag aac cgg			575
Lys Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg			
180	185	190	
gac cag gtg atc gaa gcg ttt cga gat ttc gtc gcc ggt ttc ccg cac			623
Asp Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His			
195	200	205	
gta atc ccc aag tac ata aac cga ctg aga gcg atc aga gac ata ctg			671
Val Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu			
210	215	220	
gtg aac tcc aag ttt ttc act acg cac gag gtg atc ggc agc tcg ctg			719
Val Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu			
225	230	235	
ctg ttc gtg cac gac agc aag aac gcc aac ata tgg ctt atc gac ttc			767
Leu Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe			
240	245	250	255
gca aag acg ctc ata ctt ccg ccg gac atc cgg atc aac cac acg tcc			815
Ala Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser			
260	265	270	
gag tgg gtg gtg ggc aac cac gag gac ggt tac ctg atc ggt atc aac			863
Glu Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn			
275	280	285	
aac ctg ctg gac ata ttc acc gat atg aac gcc gcc acc gcg ttt ccc			911
Asn Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro			
290	295	300	
gtc acg ctc atc gaa gtc acg gcc ccg tcc gaa gtc acc tga			953
Val Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr *			
305	310	315	
acgccgtcga tccccgccgg taccctgact cgctcggcga cccactcgcc ggtgtcattc			1013
gattccagcc acccactcag tgggtcttgcg aatcacgtga cccaccccggt tgacaatgtg			1073
tgataataat aatatgtctg gcgcaaaaata ttccaaaaaag tctttttttaa attacacttt			1133
cgatttttcga cgacaaacaa aatgacgcgcg ttttccgtac ctacctactg taggggttcgt			1193
tccgattgca atcataattt attttacccc caccacaacc ccgaaccggt tatggccac			1253
cagaggattt gccatcagta ttaaaacaat gatctattat agatgttaaa aaataaatat			1313
tatataatta tacatcatcg cggtgtgttg tgtaatatgc ctattataat atgtactata			1373
ttatacacat agcatattat aaaaatagta tattattata ttatattata ataattattat			1433

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ggttatgtgt gtttgtgtgg aaatccaata atataaaata atagttatta tttttaaata 1493
ctgtgtacgat aatgggacta ctacgtgtga ttctcaaagt atatatatat attaataattt 1553
taaacgtaca tttttaattc caaacgtata tgacgtgtgt atatatattt atgatataat 1613
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ttatttcctc acgaaaacga gaagtcctca tttctttctc ccgttacagt gtgtgtgtgt 1973
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcgtatgtgt atgtgtgaaa tttttgattt 2033
aattatatat tattataatt ttttctcctt atatttttat ttattattat aacatttttt 2093
ttgtgtgtac agaattttta aataagactt gtaaaagaaa cccttgttat attattttat 2153
tttttatttc acttcgcaca tgtgtacata ataaatcggt atcgcccttaa aaaaaaaaaa 2213
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2270

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<210> 25
 <211> 316
 <212> PRT
 <213> Zea mays

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<400> 25
Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe Phe
 1          5          10          15
Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly His
          20          25          30
Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys
          35          40          45
Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val
          50          55          60
Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp
65          70          75          80
Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser
          85          90          95
Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu
          100          105          110
Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr
          115          120          125
Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His
          130          135          140
Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr
145          150          155          160
Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys
          165          170          175
Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp
          180          185          190
Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val
          195          200          205
Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val
          210          215          220
Asn Ser Lys Phe Phe Thr His Glu Val Ile Gly Ser Ser Leu Leu
225          230          235          240
Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala
          245          250          255
Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu
          260          265          270
Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn
          275          280          285
Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro Val

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290 295 300
 Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr
 305 310 315

<210> 26
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(25)

<400> 26
 accgcttcca ccatcgccac tcgtc 25

<210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(30)

<400> 27
 ccttagacgc agcctttggg tccttcttaa 30

<210> 28
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(36)

<400> 28
 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa 36

<210> 29
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 29
 Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu
 1 5 10 15
 Asp Leu Lys Met Gly
 20

<210> 30
 <211> 33

<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(33)
<223> Xaa = Any Amino Acid

<400> 30
Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
1 5 10 15
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
20 25 30
Gln

<210> 31
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(33)
<223> Xaa = Any Amino Acid

<400> 31
Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
1 5 10 15
Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
20 25 30
Gln

<210> 32
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(33)
<223> Xaa = Any Amino Acid

<400> 32
Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
1 5 10 15
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
20 25 30
Gln

<210> 33
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(33)
 <223> Xaa = Any Amino Acid

<400> 33
 Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
 1 5 10 15
 Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu
 20 25 30
 Gln

<210> 34
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence
 <221> VARIANT
 <222> (1)...(41)
 <223> Xaa = Any Amino Acid

<400> 34
 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp
 1 5 10 15
 Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr
 20 25 30
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
 35 40

<210> 35
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(41)
 <223> Xaa = Any Amino Acid

<400> 35

Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp
 1 5 10 15
 Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr
 20 25 30
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
 35 40

<210> 36
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
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<221> VARIANT
 <222> (1)...(41)
 <223> Xaa = Any Amino Acid

<400> 36
 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp
 1 5 10 15
 Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr
 20 25 30
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
 35 40

<210> 37
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(41)
 <223> Xaa = Any Amino Acid

<400> 37
 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp
 1 5 10 15
 Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr
 20 25 30
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
 35 40